



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:40 pm GMT

PDB ID : 4V4B
EMDB ID: : EMD-1067
Title : Structure of the ribosomal 80S-eEF2-sordarin complex from yeast obtained by docking atomic models for RNA and protein components into a 11.7 Å cryo-EM map.
Authors : Spahn, C.M.; Gomez-Lorenzo, M.G.; Grassucci, R.A.; Jorgensen, R.; Andersen, G.R.; Beckmann, R.; Penczek, P.A.; Ballesta, J.P.G.; Frank, J.
Deposited on : 2004-01-06
Resolution : 11.70 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

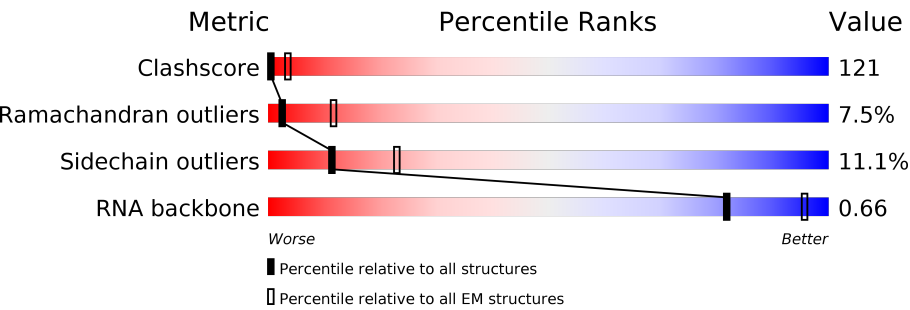
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 11.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



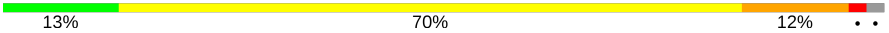
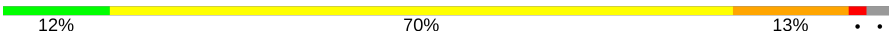
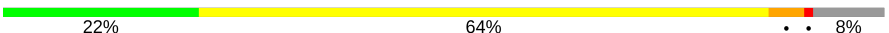


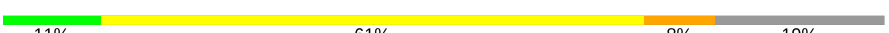
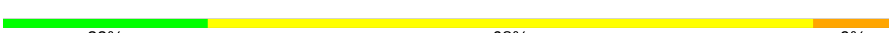




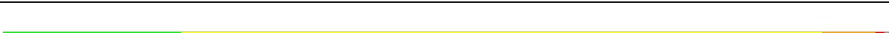


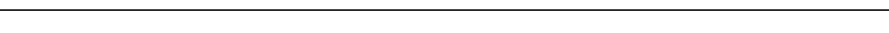




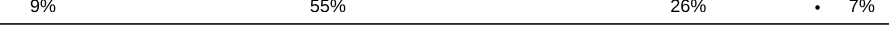

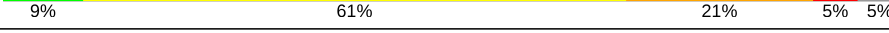



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	AA	1507	<div><div>26%</div><div>59%</div><div>11%</div><div>.</div><div>.</div></div>
2	AT	842	<div><div>62%</div><div>33%</div><div>.</div><div>.</div></div>
3	AB	185	<div><div>23%</div><div>69%</div><div>7%</div><div>.</div></div>
4	AC	192	<div><div>27%</div><div>60%</div><div>11%</div><div>.</div><div>.</div></div>
5	AD	179	<div><div>18%</div><div>72%</div><div>9%</div><div>.</div></div>
6	AE	149	<div><div>24%</div><div>70%</div><div>5%</div></div>
7	AG	150	<div><div>25%</div><div>67%</div><div>8%</div></div>
8	AH	129	<div><div>19%</div><div>71%</div><div>8%</div><div>.</div></div>


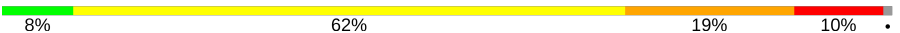
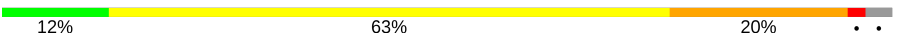

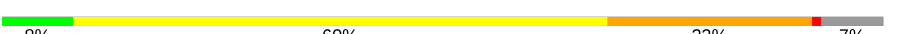
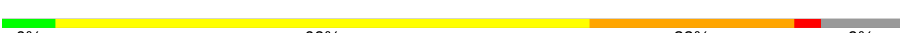






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Mol	Chain	Length	Quality of chain
9	AI	142	
10	AJ	100	
11	AK	136	
12	AL	118	
13	AM	132	
14	AN	36	
15	AO	65	
16	AQ	76	
17	AS	80	
18	B3	2999	
19	B4	125	
20	BA	217	
21	BB	253	
22	BC	386	
23	BD	361	
24	BE	222	
25	BF	162	
26	BG	119	
27	BH	191	
28	BI	168	
29	BJ	173	
30	BK	131	
31	BL	203	
32	BM	146	
33	BN	183	

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Mol	Chain	Length	Quality of chain
34	BO	120	
35	BP	142	
36	BQ	100	
37	BR	137	
38	BS	56	
39	BT	83	
40	BU	126	
41	BV	148	
42	B0	130	
43	BW	112	
44	BX	120	
45	BY	87	
46	BZ	105	
47	B9	91	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 146792 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1466	Total	C	N	O	P	0	0
			31507	14026	5840	10176	1465		

- Molecule 2 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AT	819	Total	C	N	O	S	0	0
			6375	4057	1086	1202	30		

- Molecule 3 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	185	Total	C	N	O	S	0	0
			1438	919	261	256	2		

- Molecule 4 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	188	Total	C	N	O	S	0	0
			1469	929	271	263	6		

- Molecule 5 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AD	178	Total	C	N	O	S	0	0
			1424	893	271	259	1		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	149	Total	C	N	O	S	0	0
			1099	691	206	200	2		

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	150	Total	C	N	O	S	0	0
			1161	714	229	215	3		

- Molecule 8 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	127	Total	C	N	O	S	0	0
			1004	640	183	178	3		

- Molecule 9 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	139	Total	C	N	O	S	0	0
			1094	700	201	193			

- Molecule 10 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	97	Total	C	N	O	S	0	0
			777	492	141	143	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AJ	?	-	VAL	DELETION	UNP P38701

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	125	Total	C	N	O	S	0	0
			925	566	181	175	3		

- Molecule 12 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	118	Total	C	N	O	S	0	0
			906	579	166	159	2		

- Molecule 13 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	131	Total	C	N	O	S	0	0
			1084	675	218	189	2		

- Molecule 14 is a protein called 40S ribosomal protein S29-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	29	Total	C	N	O	S	0	0
			235	141	48	42	4		

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	65	Total	C	N	O	S	0	0
			552	353	107	91	1		

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	76	Total	C	N	O	S	0	0
			618	396	120	100	2		

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS	80	Total	C	N	O	S	0	0
			622	398	110	108	6		

- Molecule 18 is a RNA chain called 5.8S/25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B3	2863	Total	C	N	O	P	0	69
			59964	26726	11030	19346	2862		

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B3	73	C	U	CONFLICT	GB 3377778
B3	74	A	G	CONFLICT	GB 3377778
B3	103	U	C	CONFLICT	GB 3377778
B3	104	G	A	CONFLICT	GB 3377778
B3	?	-	U	DELETION	GB 3377778
B3	?	-	C	DELETION	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	130	C	-	INSERTION	GB 3377778
B3	131B	U	-	INSERTION	GB 3377778
B3	200	U	C	CONFLICT	GB 3377778
B3	300	C	U	CONFLICT	GB 3377778
B3	301	G	C	CONFLICT	GB 3377778
B3	318	C	U	CONFLICT	GB 3377778
B3	350	C	G	CONFLICT	GB 3377778
B3	351	G	A	CONFLICT	GB 3377778
B3	363	A	C	CONFLICT	GB 3377778
B3	364	C	U	CONFLICT	GB 3377778
B3	560	C	U	CONFLICT	GB 3377778
B3	574	C	G	CONFLICT	GB 3377778
B3	575	G	A	CONFLICT	GB 3377778
B3	582	C	U	CONFLICT	GB 3377778
B3	583	G	C	CONFLICT	GB 3377778
B3	653	C	U	CONFLICT	GB 3377778
B3	972	C	-	INSERTION	GB 3377778
B3	973	U	-	INSERTION	GB 3377778
B3	974	A	-	INSERTION	GB 3377778
B3	976Z	G	-	INSERTION	GB 3377778
B3	976	G	-	INSERTION	GB 3377778
B3	977	G	-	INSERTION	GB 3377778
B3	978	G	-	INSERTION	GB 3377778
B3	979	G	-	INSERTION	GB 3377778
B3	980	C	-	INSERTION	GB 3377778
B3	981	C	-	INSERTION	GB 3377778
B3	982	C	-	INSERTION	GB 3377778
B3	983	A	-	INSERTION	GB 3377778
B3	984	C	-	INSERTION	GB 3377778
B3	985	C	-	INSERTION	GB 3377778
B3	986	A	-	INSERTION	GB 3377778
B3	987	G	-	INSERTION	GB 3377778
B3	988	C	-	INSERTION	GB 3377778
B3	989	C	-	INSERTION	GB 3377778
B3	990	U	-	INSERTION	GB 3377778
B3	991	A	-	INSERTION	GB 3377778
B3	992	C	-	INSERTION	GB 3377778
B3	993	C	-	INSERTION	GB 3377778
B3	994	A	-	INSERTION	GB 3377778
B3	995	A	-	INSERTION	GB 3377778
B3	1026	C	U	CONFLICT	GB 3377778
B3	1162	U	G	CONFLICT	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	1165	U	G	CONFLICT	GB 3377778
B3	1166	G	A	CONFLICT	GB 3377778
B3	1180	C	U	CONFLICT	GB 3377778
B3	1182	U	C	CONFLICT	GB 3377778
B3	1184	A	C	CONFLICT	GB 3377778
B3	1186	U	C	CONFLICT	GB 3377778
B3	1190	A	G	CONFLICT	GB 3377778
B3	1191	G	A	CONFLICT	GB 3377778
B3	1193	G	A	CONFLICT	GB 3377778
B3	1194	U	A	CONFLICT	GB 3377778
B3	1206	C	U	CONFLICT	GB 3377778
B3	1320	U	C	CONFLICT	GB 3377778
B3	1326	U	C	CONFLICT	GB 3377778
B3	1329	A	G	CONFLICT	GB 3377778
B3	1331	A	G	CONFLICT	GB 3377778
B3	1337	A	G	CONFLICT	GB 3377778
B3	1479	A	G	CONFLICT	GB 3377778
B3	1480	U	A	CONFLICT	GB 3377778
B3	1496	G	A	CONFLICT	GB 3377778
B3	1587	U	A	CONFLICT	GB 3377778
B3	1669	A	G	CONFLICT	GB 3377778
B3	1670	G	A	CONFLICT	GB 3377778
B3	1949	C	G	CONFLICT	GB 3377778
B3	1950	C	G	CONFLICT	GB 3377778
B3	1959	A	G	CONFLICT	GB 3377778
B3	1962	G	C	CONFLICT	GB 3377778
B3	1963	G	C	CONFLICT	GB 3377778
B3	1966	C	U	CONFLICT	GB 3377778
B3	2137	U	A	CONFLICT	GB 3377778
B3	2139	U	G	CONFLICT	GB 3377778
B3	3145	G	-	INSERTION	GB 3377778
B3	2146	G	-	INSERTION	GB 3377778
B3	2147	G	-	INSERTION	GB 3377778
B3	2148	G	-	INSERTION	GB 3377778
B3	2149	A	-	INSERTION	GB 3377778
B3	2150	U	-	INSERTION	GB 3377778
B3	2151	G	-	INSERTION	GB 3377778
B3	2152	C	-	INSERTION	GB 3377778
B3	2153	G	-	INSERTION	GB 3377778
B3	2154	U	-	INSERTION	GB 3377778
B3	2155	A	-	INSERTION	GB 3377778
B3	2156	G	-	INSERTION	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	2157	G	-	INSERTION	GB 3377778
B3	2158	A	-	INSERTION	GB 3377778
B3	2159	U	-	INSERTION	GB 3377778
B3	2160	A	-	INSERTION	GB 3377778
B3	2161	G	-	INSERTION	GB 3377778
B3	2162	G	-	INSERTION	GB 3377778
B3	2163	U	-	INSERTION	GB 3377778
B3	2164	G	-	INSERTION	GB 3377778
B3	2165	G	-	INSERTION	GB 3377778
B3	2166	G	-	INSERTION	GB 3377778
B3	2167	A	-	INSERTION	GB 3377778
B3	2168	G	-	INSERTION	GB 3377778
B3	2169	C	-	INSERTION	GB 3377778
B3	2170	G	-	INSERTION	GB 3377778
B3	2171	C	-	INSERTION	GB 3377778
B3	2203	A	-	INSERTION	GB 3377778
B3	2204	A	-	INSERTION	GB 3377778
B3	2205	G	-	INSERTION	GB 3377778
B3	2206	C	-	INSERTION	GB 3377778
B3	2207	G	-	INSERTION	GB 3377778
B3	2208	C	-	INSERTION	GB 3377778
B3	2209	C	-	INSERTION	GB 3377778
B3	2210	G	-	INSERTION	GB 3377778
B3	2211	G	-	INSERTION	GB 3377778
B3	2212	U	-	INSERTION	GB 3377778
B3	2213	G	-	INSERTION	GB 3377778
B3	2214	A	-	INSERTION	GB 3377778
B3	2215	A	-	INSERTION	GB 3377778
B3	2216	A	-	INSERTION	GB 3377778
B3	2217	U	-	INSERTION	GB 3377778
B3	2218	A	-	INSERTION	GB 3377778
B3	2219	C	-	INSERTION	GB 3377778
B3	2220	C	-	INSERTION	GB 3377778
B3	2221	A	-	INSERTION	GB 3377778
B3	2222	C	-	INSERTION	GB 3377778
B3	2223	C	-	INSERTION	GB 3377778
B3	2224	C	-	INSERTION	GB 3377778
B3	2225	U	-	INSERTION	GB 3377778
B3	2226	U	-	INSERTION	GB 3377778
B3	2227	C	-	INSERTION	GB 3377778
B3	2228	C	-	INSERTION	GB 3377778
B3	2229	C	-	INSERTION	GB 3377778

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Chain	Residue	Modelled	Actual	Comment	Reference
B3	2230	C	-	INSERTION	GB 3377778
B3	2231	G	-	INSERTION	GB 3377778
B3	2232	G	-	INSERTION	GB 3377778
B3	2233	C	-	INSERTION	GB 3377778
B3	2234	U	-	INSERTION	GB 3377778
B3	2235	G	-	INSERTION	GB 3377778
B3	2236	G	-	INSERTION	GB 3377778
B3	2325	C	U	CONFLICT	GB 3377778
B3	2326	U	C	CONFLICT	GB 3377778
B3	2341	G	A	CONFLICT	GB 3377778
B3	2374	A	G	CONFLICT	GB 3377778
B3	2375	G	A	CONFLICT	GB 3377778

- Molecule 19 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	B4	122	Total	C	N	O	P	0	0
			2600	1160	472	847	121		

- Molecule 20 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BA	213	Total	C	N	O	S	0	0
			1682	1074	294	305	9		

- Molecule 21 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BB	244	Total	C	N	O	S	0	0
			1855	1156	375	323	1		

- Molecule 22 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BC	359	Total	C	N	O	S	0	0
			2856	1813	541	495	7		

- Molecule 23 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BD	256	Total	C	N	O	S	0	0
			1942	1221	374	344	3		

- Molecule 24 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BE	222	Total	C	N	O	S	0	0
			1799	1140	312	345	2		

- Molecule 25 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BF	161	Total	C	N	O	S	0	0
			1298	854	228	215	1		

- Molecule 26 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BG	119	Total	C	N	O	S	0	0
			886	566	152	166	2		

- Molecule 27 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BH	178	Total	C	N	O	S	0	0
			1410	892	259	256	3		

- Molecule 28 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BI	165	Total	C	N	O	S	0	0
			1326	834	257	228	7		

- Molecule 29 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BJ	165	Total	C	N	O	S	0	0
			1319	826	247	242	4		

- Molecule 30 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BK	131	Total	C	N	O	S	0	0
			978	613	181	182	2		

- Molecule 31 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BL	194	Total	C	N	O	S	0	0
			1637	1022	344	270	1		

- Molecule 32 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BM	146	Total	C	N	O	S	0	0
			1165	754	221	189	1		

- Molecule 33 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BN	147	Total	C	N	O		0	0
			1163	725	226	212			

- Molecule 34 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BO	120	Total	C	N	O	S	0	0
			925	595	169	160	1		

- Molecule 35 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BP	141	Total	C	N	O		0	0
			1145	714	242	189			

- Molecule 36 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BQ	97	Total	C	N	O	S	0	0
			795	505	153	134	3		

- Molecule 37 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BR	131	Total	C	N	O	S	0	0
			977	614	183	173	7		

- Molecule 38 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	BS	53	Total	C	N	O	0	0
			439	282	84	73		

- Molecule 39 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BT	77	Total	C	N	O	S	0	0
			614	395	101	116	2		

- Molecule 40 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BU	115	Total	C	N	O	0	0
			911	574	178	159		

- Molecule 41 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BV	143	Total	C	N	O	S	0	0
			1133	723	222	185	3		

- Molecule 42 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	B0	109	Total	C	N	O	S	0	0
			880	555	176	148	1		

- Molecule 43 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BW	78	Total	C	N	O	S	0	0
			654	412	132	109	1		

- Molecule 44 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BX	59	Total	C	N	O	S	0	0
			461	294	82	84	1		

- Molecule 45 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BY	52	Total	C	N	O	S	0	0
			402	245	85	68	4		

- Molecule 46 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BZ	91	Total	C	N	O	S	0	0
			740	466	150	119	5		

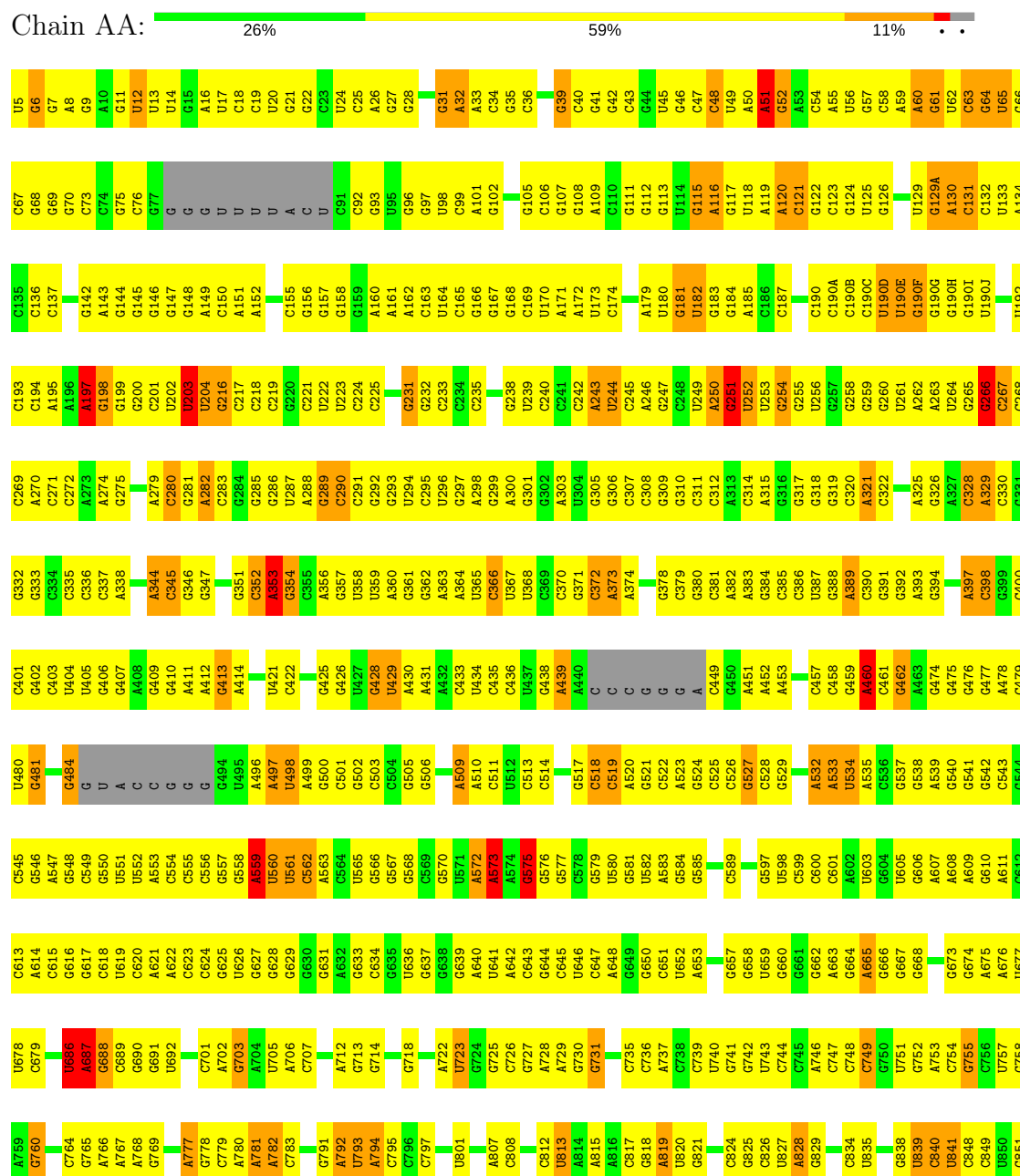
- Molecule 47 is a protein called 60S ribosomal protein L43.

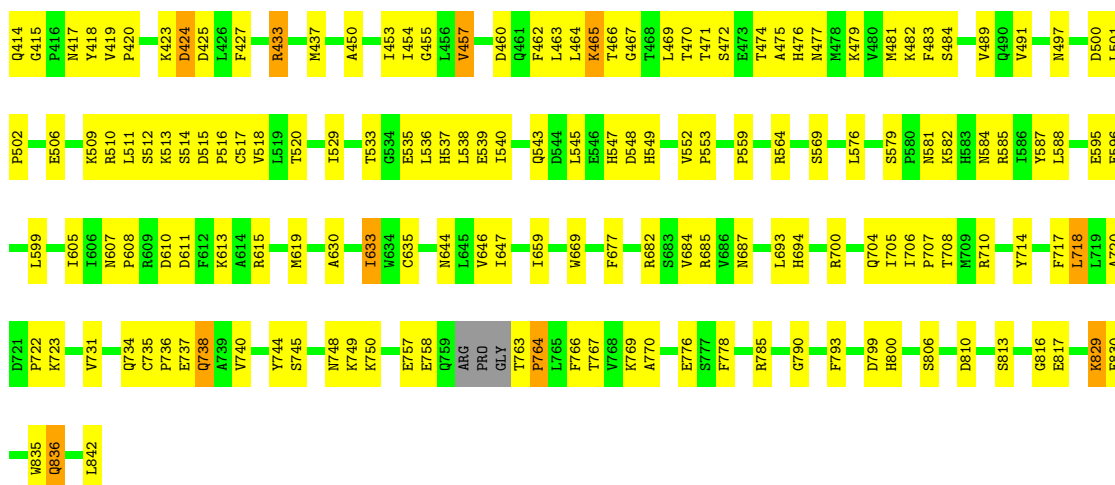
Mol	Chain	Residues	Atoms					AltConf	Trace
47	B9	73	Total	C	N	O	S	0	0
			546	338	105	98	5		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

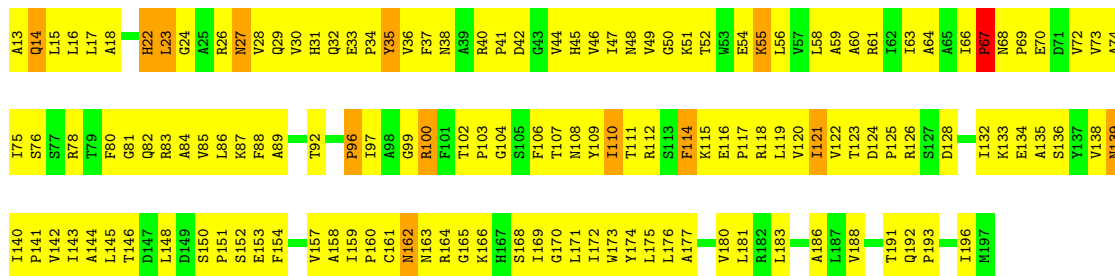
• Molecule 1: 18S ribosomal RNA





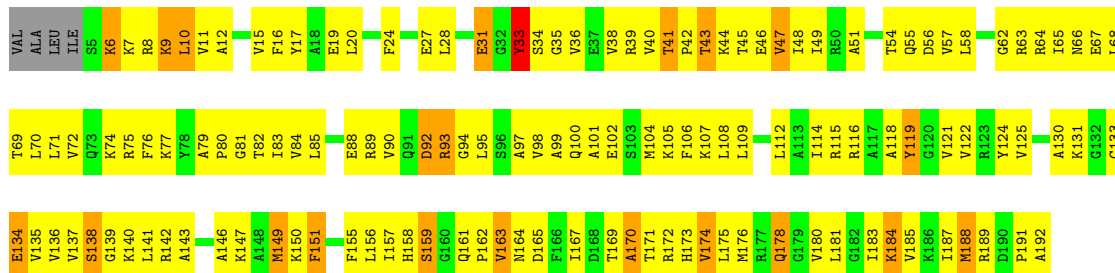
• Molecule 3: 40S ribosomal protein S0-A

Chain AB: 23% 69% 7% .



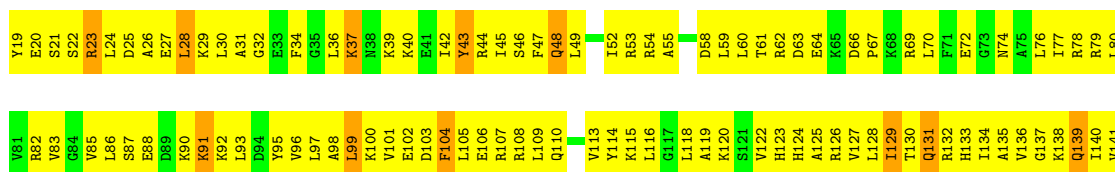
• Molecule 4: 40S ribosomal protein S3

Chain AC: 27% 60% 11% .



• Molecule 5: 40S ribosomal protein S9-A

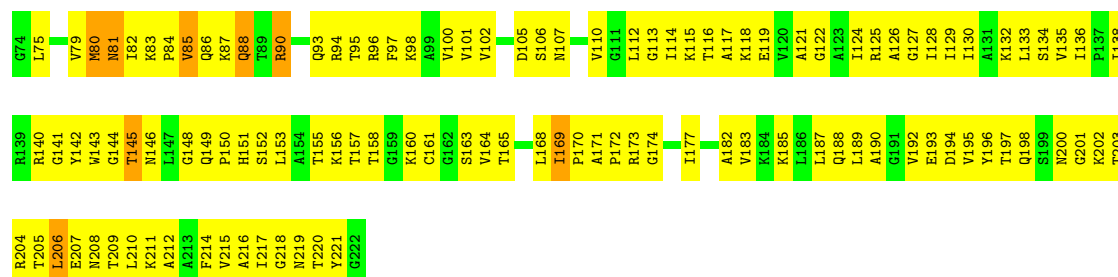
Chain AD: 18% 72% 9% .





• Molecule 6: 40S ribosomal protein S2

Chain AE: 24% 70% 5%



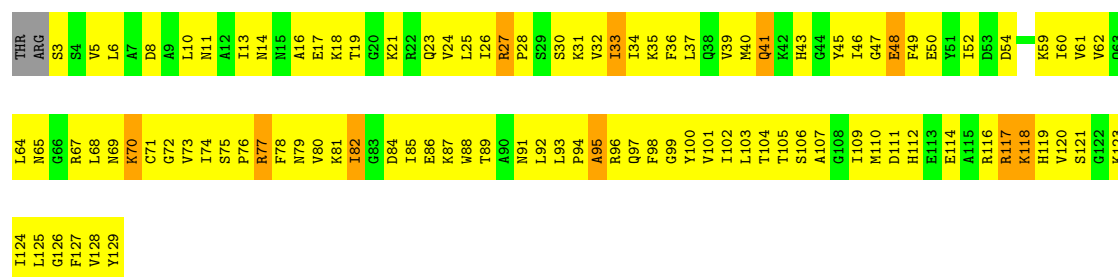
• Molecule 7: 40S ribosomal protein S5

Chain AG: 25% 67% 8%



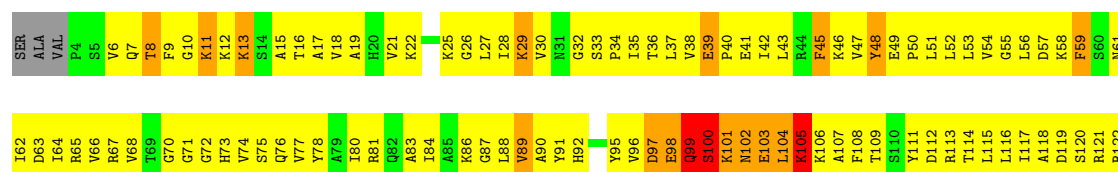
• Molecule 8: 40S ribosomal protein S22

Chain AH: 19% 71% 8%



• Molecule 9: 40S ribosomal protein S16

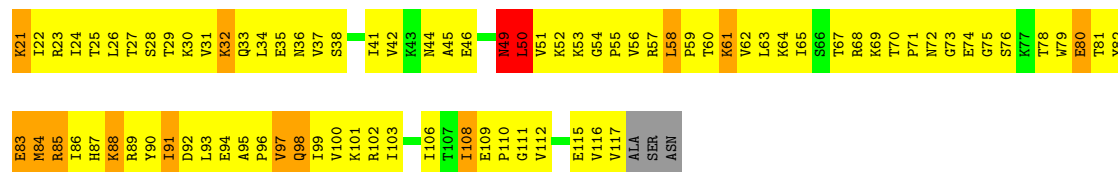
Chain AI: 13% 70% 12%





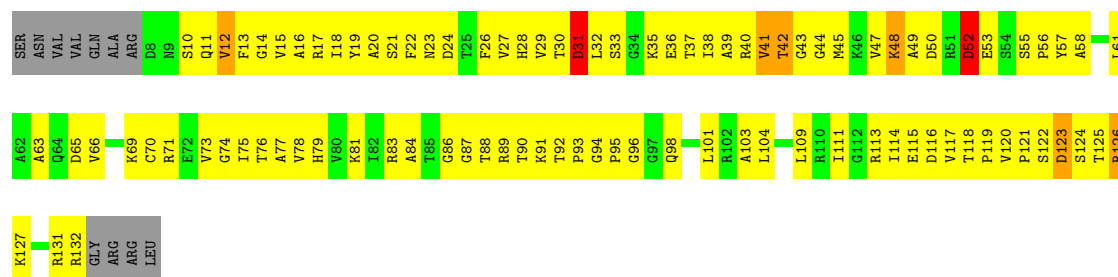
• Molecule 10: 40S ribosomal protein S20

Chain AJ: 12% 70% 13% . .



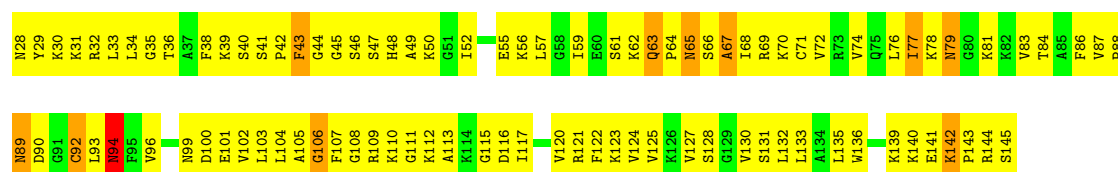
• Molecule 11: 40S ribosomal protein S14-A

Chain AK: 22% 64% . . 8%



• Molecule 12: 40S ribosomal protein S23

Chain AL: 19% 71% 8% .




• Molecule 13: 40S ribosomal protein S18

Chain AM: 14% 81% 5% .



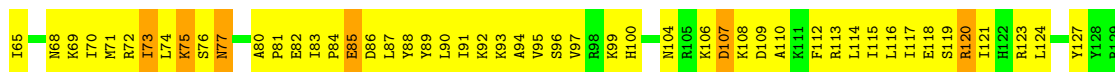
• Molecule 14: 40S ribosomal protein S29-B

Chain AN: 



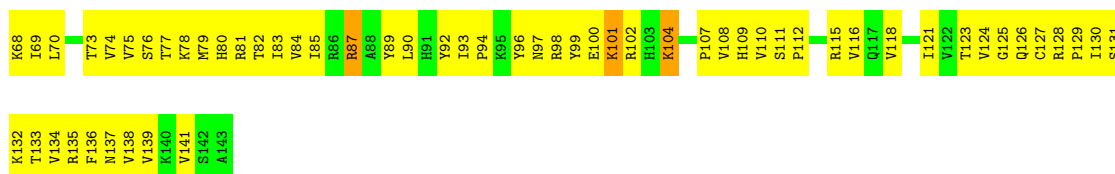
- Molecule 15: 40S ribosomal protein S13

Chain AO:  23% 68% 9%



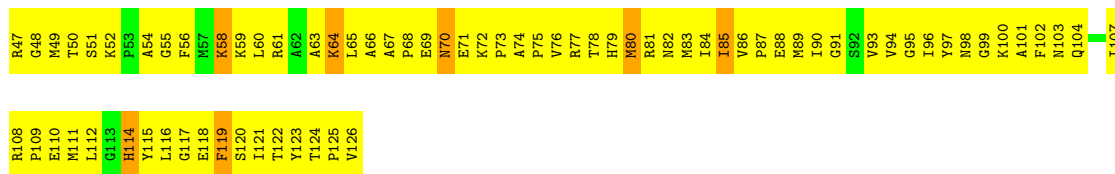
- Molecule 16: 40S ribosomal protein S11

Chain AQ: 24% 72% .



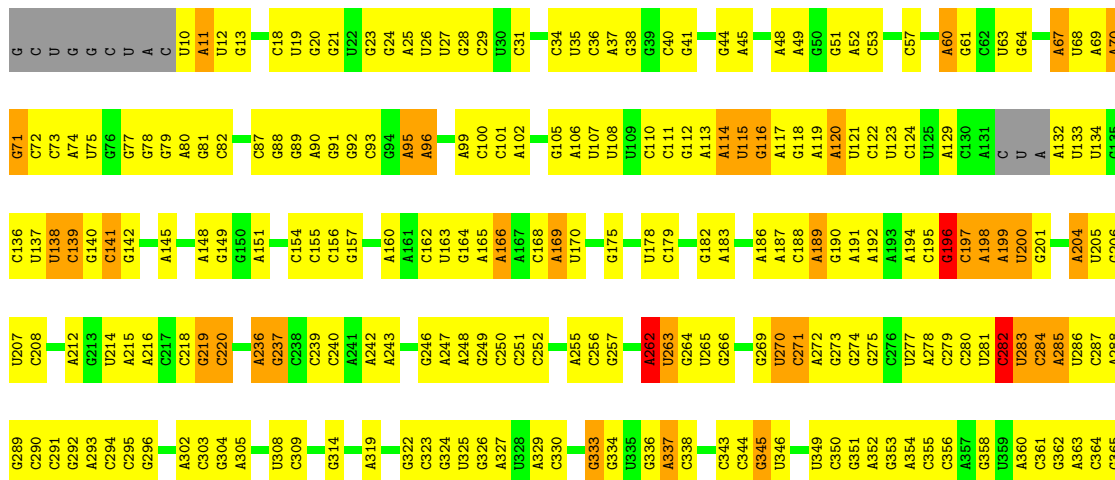
- Molecule 17: 40S ribosomal protein S15

Chain AS: 9% 83% 9%



- Molecule 18: 5.8S/25S ribosomal RNA

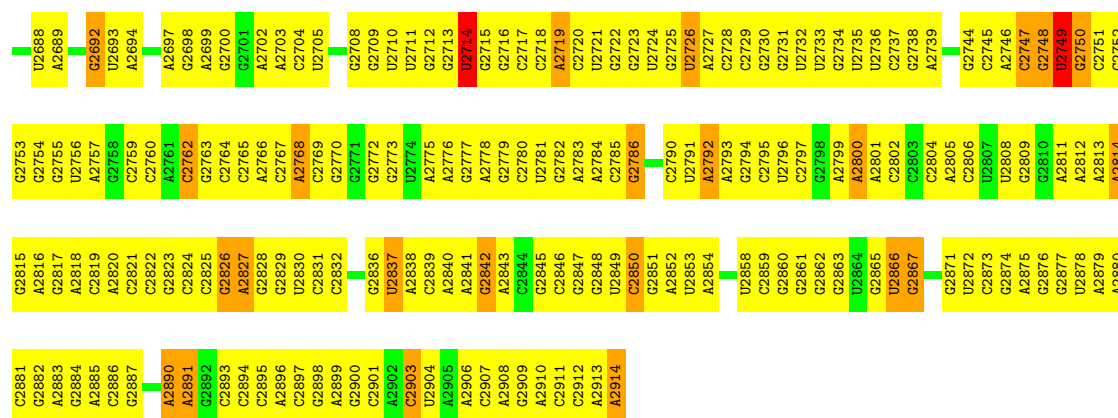
Chain B3:  33% 53% 9% 5%



U1473	C1400	U1333	A1259	A1192	A1124	G1052	C	A907	A819	G745	A665	U595	A520	A441	U366
C1474	G1334	G1260	A1281	G1193	U1125	G1053	C	A908	G820	G746	A666	C596	A521		G367
	C1335	A1282	A1281	U1194	G1126	G1054	C		U821	A746	C667	C597	U522	U445	C368
C1477	U1336	C1262	G1195	G1195	G1127	U1055	A	U918		G747		C598	C523	U446	G370
U1478	A1406	A1337	C1263	C1196	U1128	U1056	C	U919	G834	G748	G670	C599	A524	A447	
	U1338				C1129	A1057	C	C920	U835	C749	A671	C600	G525	G448	U371
A1485	G1339	C1287	C1339	A1199	U1130	A1058	G	A922	G836	G750	G672	A602	U526	A449	A372
	U1409	C1288	G1340	C1268	G1131	G1059	C	G921				G603	U527	C450	G373
U1488		C1289	C1269	C1201	A1132	C1061	A	A923	G841	G754		A604	G528	C451	U374
	A1414	C1342	C1342	A1202	A1133	U1062	C	G924				G605	G529	C452	G375
A1492	G1415	C1343			G1134	U1063	U	C925	C842		C677		G528	A453	C376
A1493	A1344	C1273		C1206		G1063	C	A926	A843	C759			A532		C377
A1494	A1345			A1207	G1137	U1064	G		A844	G760	G679	U612		U457	A378
C1495	U1346	C1277		C1208	G1138	G1065	C	C934	U845	A761	G680	C513	G535		A379
A1496	A1278	A1278	A1278	C1209	U1139	U1066	C	G935	A846	C762	G681	U614	A536	C461	G380
G1497	U1279	U1279	U1279	G1210	C1140	A1067	A		C847	C763	A682	G615	G537	C461	G381
	G1349	G1211		G1210	U1141			G938	C848	C764	G683	U616	C538	C471	U382
A1501	A1280	C1212		C1212	C1142		C	A939	C849	C765	G684	C517	G539	A472	A383
	U1350	G1213		C1213	G1143	G1072	C	G940	U850	A766	C685	G618	A540	A473	G384
U1502	G1283	G1213		C1213	G1143	A1073		G941	C951	A767		U619	C541	C474	
U1503	A1214	G1214		C1214		G1074		U942			A688	A620	A542	C475	G389
A1504	C1352	U1284		G1215	C1147		C999	A943	U855	G771		G621	G543	C476	G390
U1505	U1285	U1285		A1216	A1148	C1080	C	G944			A683	G622	G544		G391
U1506	A1286	G1364		G1217	U1149	A1081	C	U945	G856	A772	C694	U624	G545	C480	U392
U1507	A1355	A1287		U1218	A1150	G1002	C	U946	A857	A773		U625		U481	G393
C1507	A1356	U1288		U1219		U1003		G946	U858	C774	G696	U626	U548	C483	G394
U1508	A1357	C1289		G1151		C1085		U947	C959	G775	C697	U626	C550	A484	A395
G1433	U1290	G1290		U1220	A1152	A1086		U948		A776		G627	C551	A485	U396
A1434				G1221	C1153	G1087	C	U949	G868	C777		A628	A551	A486	U397
	G1295	G1295		A1222	A1154	A1088		G950	G869	U778		A529	A552	C487	U398
G1438	C1361	U1368		G1223	G1155	G1089				U779		U701	G553	U488	C399
C1439	U1362	U1298		G1224	C1156	A1090	C	A951	A700			A630	G554	C492	U401
U1440	G1363	G1299		G1225	C1157	U1091	C	G952	G873	G782		U702	G555	C492	U402
C1516	G1441	G1363		G1226	U1158	A1092	C	G953	A874	G783		G632	U555	U493	
U1517	U1517	C1301		C1227	G1159	G1093		U954	A875	A784		C633	C556	C493	
						G1094		A955	A876			G634	C557	C494	
G1445	U1367	A1368		C1228	G1160	C1015	A1014	G956	G877	A790		A635	C558	C495	A407
U1519	U1368	C1368		C1229		U1095	C	U1016	G878			G636	U559	C496	
G1520	A1369	A1230		G1163		U1096	C	A957		A791		A637	C560	A497	A410
C1521	U1446	C1305		U1164		A1097		G958	C881	G792	A708	C538	G561	A498	A411
A1448	A1448	A1307		U1165	U1165	A1098	C	C959	A882	G793	G709	C538	A562	C499	G412
G1449	G1449	A1308		A1233	G1166	G1099	C1019	G960	U883	A794	G710	A639		G500	G413
C1450	C1377	U1309		U1234	G1167	G1100	A1020	A961	U883	G795		G640		G501	C414
U1524	C1451	G1378		G1235	C1168		G962	C964					A566	A502	
G1525	C1451	U1310		U1236	U1169	C1103	A1022	C963	G885	A796	U713	A643	U567	A502	G417
A1526	G1452	A1379		A1236		G1104	C1023	G964	A986	G797	U714	G644	G568	C503	C418
U1527	U1453	C1380		C1237	U1170	C1105	G1024	A965	C987	A798	U	U645	A569	G504	A419
A1528	G1454	A1381		U1171	C1171	A1106	C1025	U966	U888		G716	G646		C505	U420
G1529	U1314	G1172		G1239		A1107	C1025	U967	C889	C803		U647		G506	
U1457	U1383	U1383		G1240	A1173	G1107		G968	C890	C804			G574	A507	C421
A1458	G1384	C1316		G1241	A1174	G1108	U1029	G968	C890				G575		
A1459	C1385	A1317		A1242		U1109	U1030	G969	G891					A508	
G1460	G1386	A1318		C1243		G1110	G1031	U970		A807		C553	G581	A509	U425
U1461	C1387	G1319		U1244			G975		A894	A808		U655	C582	A509	G426
C1537	U1461	U1387		U1181		A1114	G1039	G975	A895	G809		G656	G583	A511	
C1462	C1462	U1388		C1245	U1182	U1115	A1040	C986	C896	G810		G657	G584	G512	G431
A1463	U1539	A1321		A1246	C1183	U1116	A1041	G	A897	C811		C588	C585	A513	C432
U1464	A1464	A1390		A1247	U1184	U1117	U1041	U	G898	A812		G660	C586	G514	C433
		C1322		U1248	U1185	A1117	U1042	C		G730		A660	C587	A515	U434
C1391				U1248		G1118	C1043	U				G661	G588	A516	
				U1249	U1186	A1119	U1044	C				A660	C589	A517	C438
U1454	C1328	C1250		A1187	A1188	U1120	G1045	C	G902	G814		G735	G589	A517	A439
U1544	C1468	A1329		C1251	U1189	U1121	G1045	C	U904	G816		G662	U589	A517	C438
A1470	A1470	A1330		A1189	A1189	G1121	U1120	C	G905	A736		U663	C589	A518	C440
G1546	C1397	C1397		C1331	A1190	U1122	G1050	C	C905	G817		C563	C594	A519	
	C1472	A1308		C1322	A1191	A1123	G1051	U	C906	A819		U664			

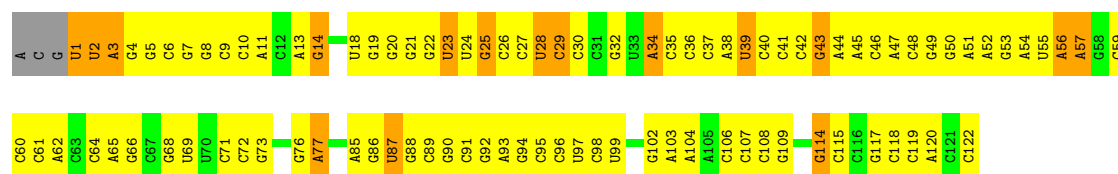
WORLDWIDE
PDB
PROTEIN DATA BANK

 **EMDataBank**
Unified Data Resource for 3DEM



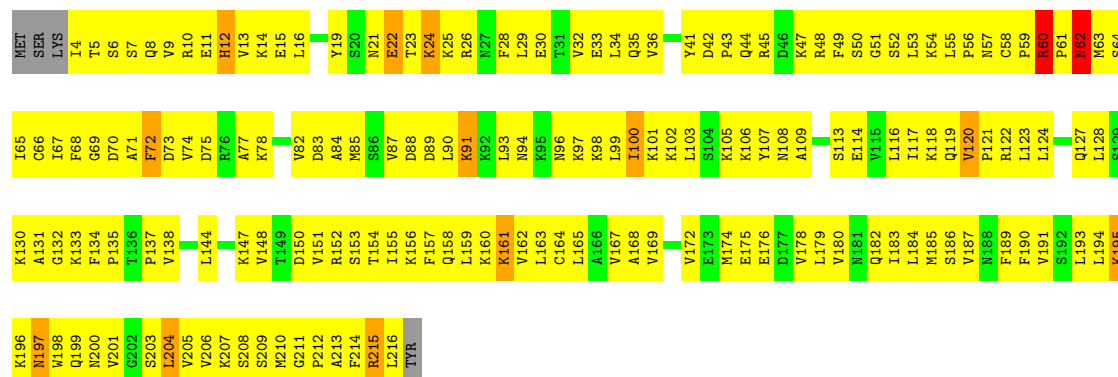
• Molecule 19: 5S RIBOSOMAL RNA

Chain B4: 22% 62% 13%



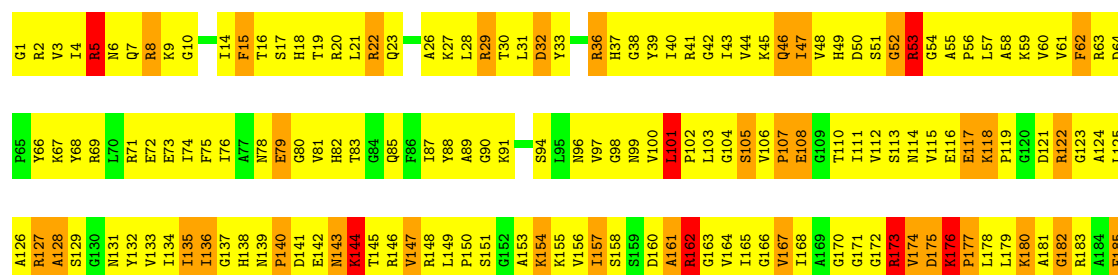
• Molecule 20: 60S ribosomal protein L1

Chain BA: 20% 72% 6%



• Molecule 21: 60S ribosomal protein L2

Chain BB: 10% 61% 21%



ARG	H186
GLY	K187
SER	Y188
GLN	R189
LYS	L190
THR	K191
GLN	R192
ASP	Y193
	S194
	Y195
	P196
	K197
	T198
	R199
	G200
	V201
	A202
	M203
	M204
	P205
	V206
	D207
	H208
	P209
	H210
	G211
	G212
	G213
	N214
	H215
	Q216
	H217
	T218
	G219
	K220
	A221
	S222
	T223
	I224
	S225
	R226
	G227
	A228
	V229
	S230
	G231
	Q232
	K233
	A234
	G235
	L236
	I237
	A238
	A239
	R240
	R241
	G242
	G243
	L244
	T245

- Molecule 22: 60S ribosomal protein L3

Chain BC: 8% 63% 19% 7%


THR	V311	L245	G184	K123	R61	SER
	V312	R246	G185	S124	P62	HIS
	ALA	R313	S186	K125	G63	ARG
	G314	V248	S187	L126	S64	LYS
	LYS	E315	A249	S188	K65	TVR
	I316	C250	E189	A128	F66	GLU
	K317	T251	K190	F129		A7
	PHE	N318	G252	T130	R69	P8
	MET	D319	A253	K131	E70	R9
	GLY	F320	R254	V132	V71	H10
THR	I321	H255	A194	S133	V72	G11
	M322	P256	R195	K134	E73	H12
	L323	A257		K135	F74	L13
	K324	H258	F198	Q138	V75	L14
	G325	V259	E199	Q139	T76	F15
	C326	M260	K200	D139	V77	L16
	I327	H261	T201	G140	V78	L17
	P328	S262	V202	A141	D79	P17
	G329	V263	A203	G142	T80	R18
		N330	R264	I143	P81	K19
LYS	R331	K265	D205	E144		R20
	K332	A266	S206	R145	P82	A21
	R333	G267	V207	E146	V84	A22
	L334	Q268	F208	L147	V85	S23
	V335	R269	E209	A148	V86	T24
	T336	G270	Q210	R149	G87	R25
	L337	Y271	M211	I150	V88	A26
	R338	H272	E212	K151	V89	R27
	K339	S273	M213	K152	G90	V28
	S340	R274	L214	L153	Y91	K29
LEU	L341	T275	D215	A154	V92	A30
	Y342	S276	A216	S155	E93	F31
	T343	L277	I217	V156	T94	P32
	N344	N278	A218	V157	P95	K33
	T345	H279	V219	R158	R96	D34
	S346	K280	T220	V159	G97	R35
	R347	L281	K221	L160	L98	R36
	K348	Y282	G222	V161	R99	S37
	A349	R283	H223	K162	S100	K38
	L350	V284	G224	T163	L101	P39
PHE	E351	G285	F225	Q164	T102	V40
	E352	K286	E226	T165	T103	A41
	V353	G287	G227	K166	V104	L42
	S354		T228	L167	M105	T43
	L355	S296	T229	T168	A106	S44
	W357	F297	H230	P169		F45
	I358	D298	R231	L170	L109	G47
	D359	R299	G232	A171	S110	Y48
	A361	K301	T234	K173	D111	R49
	S362	K302	K235	K174	E112	A50
GLY	K363	T303	K236	A175	V113	G51
	F364	T304	L237	H176	K114	M52
	G365	T305	P238	L177	R115	T53
		T306	R239	A178	R116	T54
	LYS	P306	K240	E179	F117	S55
	GLY	M307	T241	T180	Y118	V56
	ARG	G308	H242	Q181	K119	R57
	PHE	G309	R243	L182	N120	D58
		F310	C244	V182	M121	L59
	T311				Y121	D60

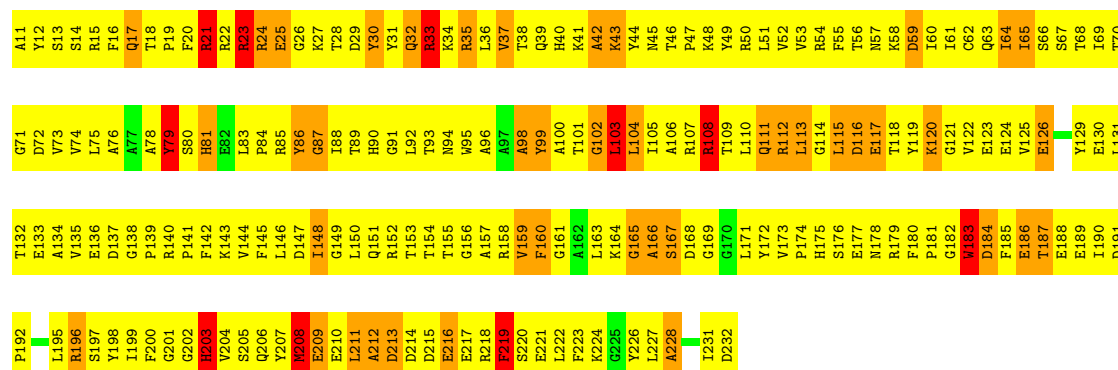
- Molecule 23: 60S ribosomal protein L4-B

Chain BD: 


GLN	L243	S183	A122	A61	SER
	G244	K184	S123	E52	ARG
	R245	X185	A124	S63	ARG
	F246	L186	I125	W64	Q4
	V247	R187	A126	G65	V5
	T248	A188	A127	T66	T6
	W249	G189	T128	G67	V7
	T250	K190	A129	R68	H8
	E251	G191	V130	A69	S9
	A252	K192	A131	V70	L10
LYS	A253	K193	S132	A71	T11
	F254	R194	L133	R72	G12
	T255	N195	V134	I73	E13
	K256	R196	L135	P74	A14
	L257	R197	A136	R75	T15
	D258	X198	R137	V76	A16
	Q259	T199	G138	G77	N17
	VAL	Q200	R139		A18
	TRP	R201	A140	G80	L19
	GLY	R202	V141	T81	P20
LEU	SER	G203		R82	L21
	GLU	P204	I144	G83	P22
	THR	L205	P145	S84	A23
	VAL	V206	E146	G85	A24
	ALA		E147	G86	F25
	ASN	Y207	P148	G87	S26
	SER	A208	L149	A88	A27
	TYR	E210	V150	F89	P28
	ALA	D211	V151	G90	R29
	VAL	N212	S152	N91	R30
PHE	GLY	G213	T153	M92	F31
	THR	L214	D154	C93	D32
	ALA	LEU	L155	R94	I33
	PRO	K216	E156	G95	V34
	SER	A217	S157	G96	H35
	HIS	L218	I158	R97	T36
	ILE	R219	Q159	M98	V37
	ILE	N220	K160	F99	F38
	SER	V221	T161	A100	T39
	LYS	P222	K162	P101	S40
ALA	SER	G223	E163	T102	V41
	ASP	V224	A164	K103	M42
	VAL	E225	V165	T104	K43
	THR	T226	A166	W105	M44
	ARG	A227	A167	K106	R45
	THR	N228	L168	K107	R46
	LYS	ILE	V229	K169	D47
	PRO	ASN	A230	N109	A48
	ALA	SER	S231	V171	V49
	ALA	SER	L232	K111	A50
VAL	GLU	N233	G172	K112	V51
	PHE	L234	H174	N113	S52
	ILE	GLN	S175	H114	F53
	SER	Q236	D176	N115	K54
	THR	ALA	L177	E116	A55
	LEU	A238	L178	K117	G56
	LYS	ARG	K179	R118	H57
	HIS	PRO	G240	V180	O58
	ASP	GLY	A241	L181	T59
			H242	V182	S60

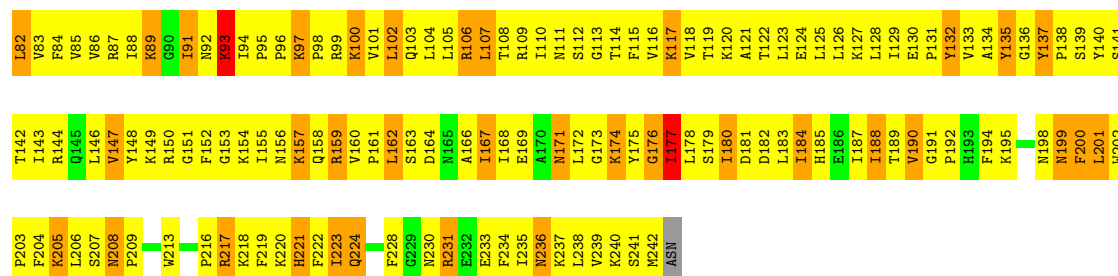
- Molecule 24: 60S ribosomal protein L5

Chain BE:  5% 71% 19% 5%




- Molecule 25: 60S ribosomal protein L7-A

Chain BF:  11% 65% 22% ..




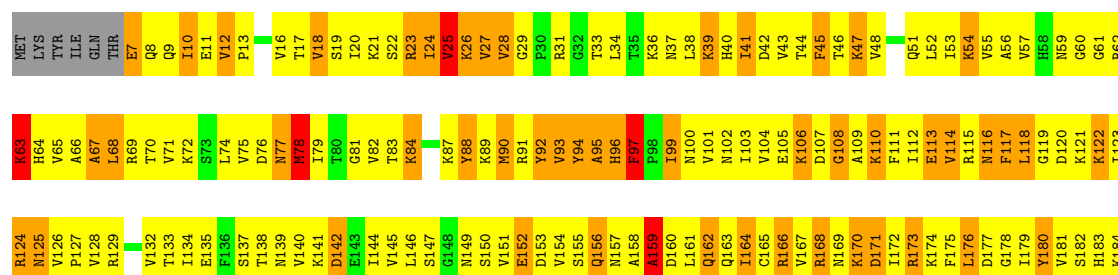
- Molecule 26: 60S ribosomal protein L8-A

Chain BG:  10% 66% 21% .

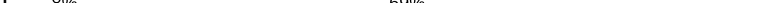


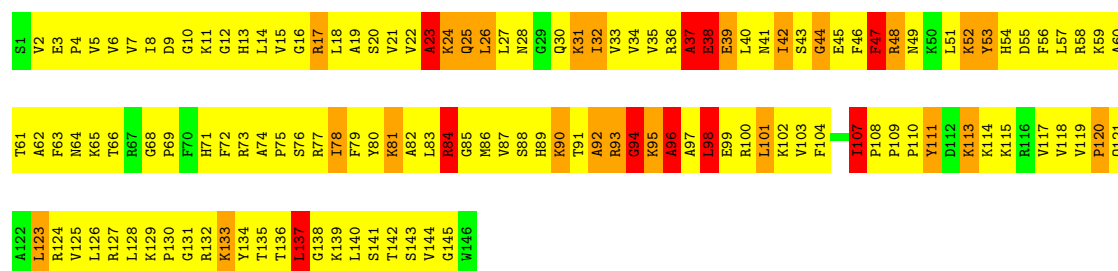
- Molecule 27: 60S ribosomal protein L9-A

Chain BH:  9% 55% 26% • 7%



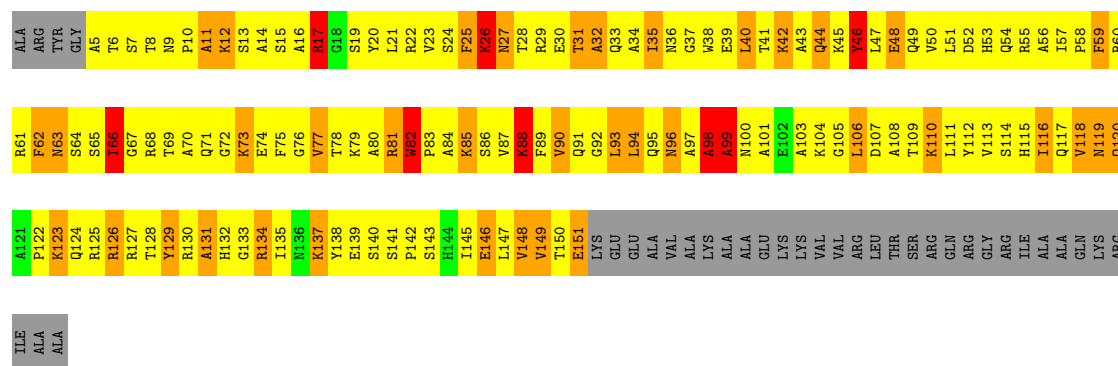
- Molecule 32: 60S ribosomal protein L16-A

Chain BM:  8% 69% 16% 7%



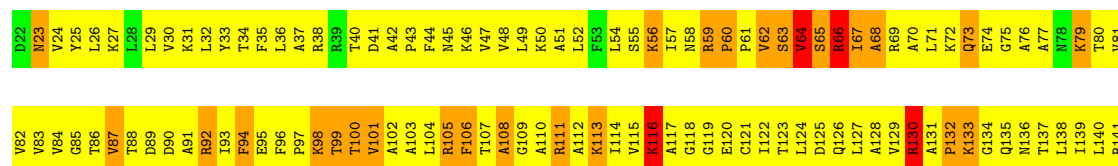
- Molecule 33: 60S ribosomal protein L17-A

Chain BN:  52% 21% 20%




- Molecule 34: 60S ribosomal protein L18

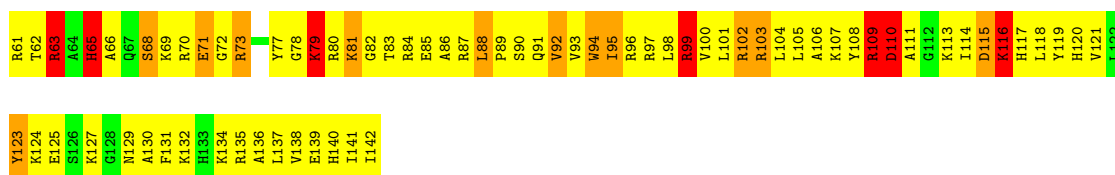
Chain BO: 72% 21%



- Molecule 35: 60S ribosomal protein L19

Chain BP: 





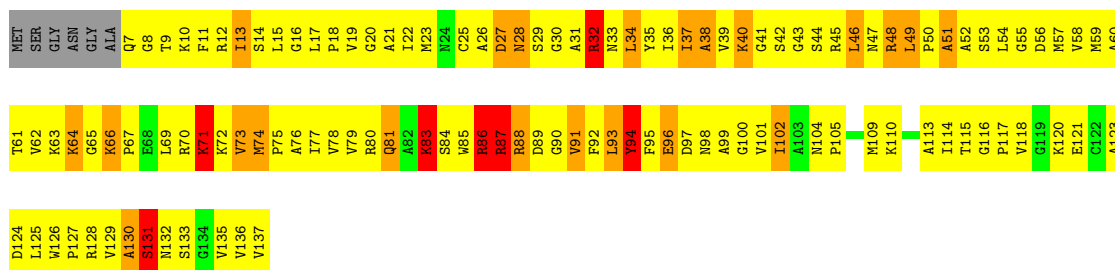
- Molecule 36: 60S ribosomal protein L21-A

Chain BQ: 12% 63% 20%



- Molecule 37: 60S ribosomal protein L23

Chain BR: 9% 66% 16% 5%



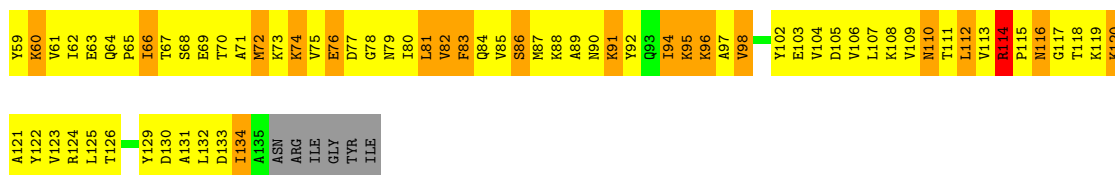
- Molecule 38: 60S ribosomal protein L24-A

Chain BS: 13% 50% 27% 5% 5%



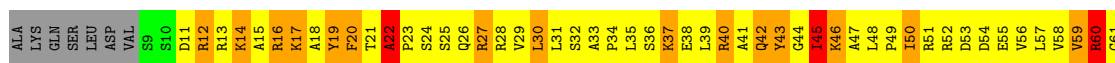
- Molecule 39: 60S ribosomal protein L25

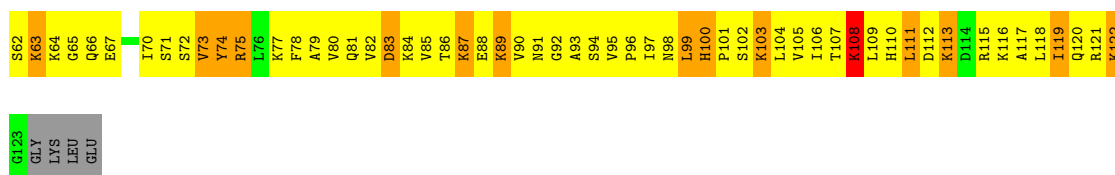
Chain BT: 8% 60% 23% 7%



- Molecule 40: 60S ribosomal protein L26-A

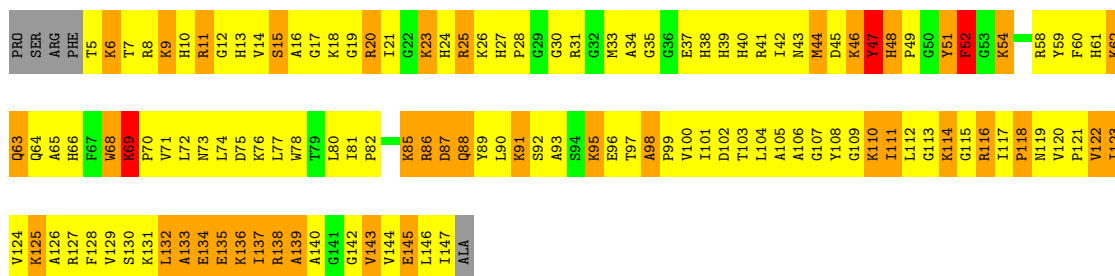
Chain BU: 6% 60% 23% 9%





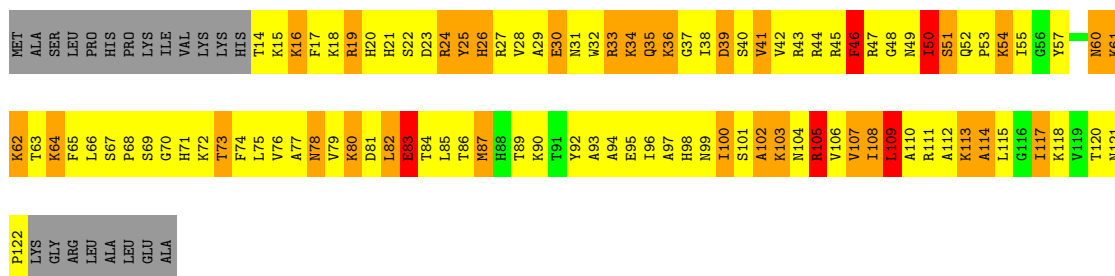
- Molecule 41: 60S ribosomal protein L28

Chain BV: 10% 57% 27%



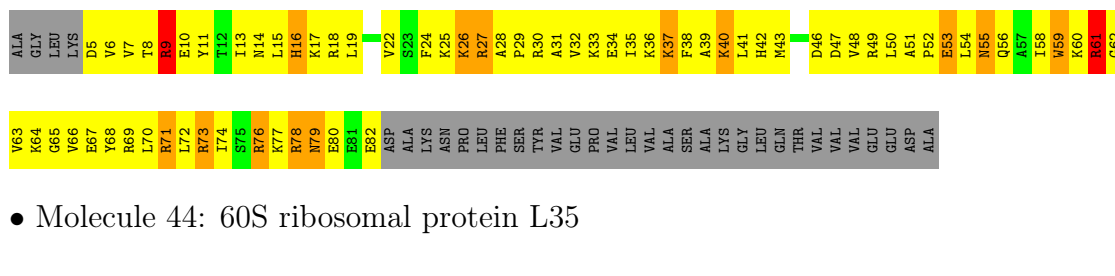
- Molecule 42: 60S ribosomal protein L32

Chain B0: 5% 51% 24% 16%



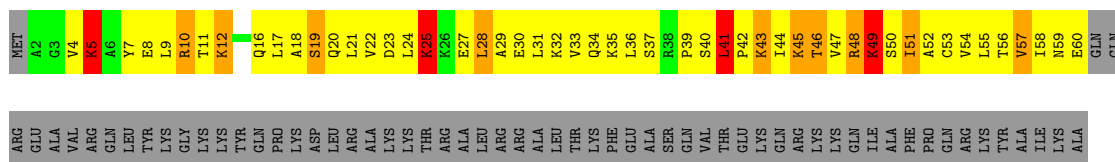
- Molecule 43: 60S ribosomal protein L31

Chain BW: 8% 48% 12% 30%



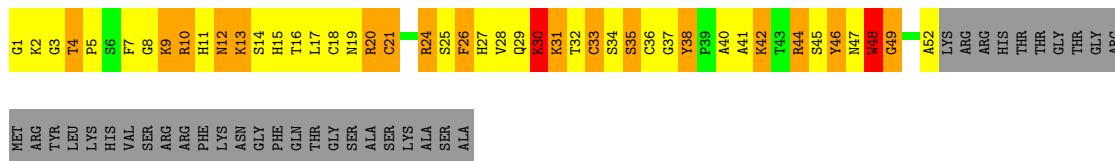
- Molecule 44: 60S ribosomal protein L35

Chain BX: 7% 31% 8% 51%




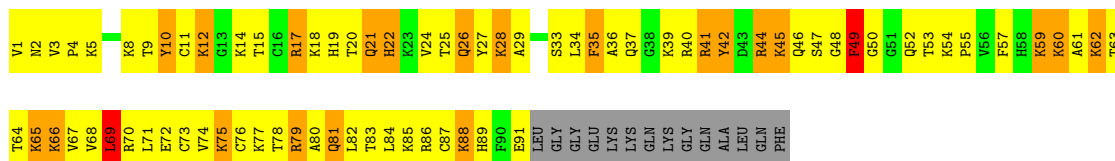
- Molecule 45: 60S ribosomal protein L37-A

Chain BY:  8% 30% 20% • 40%



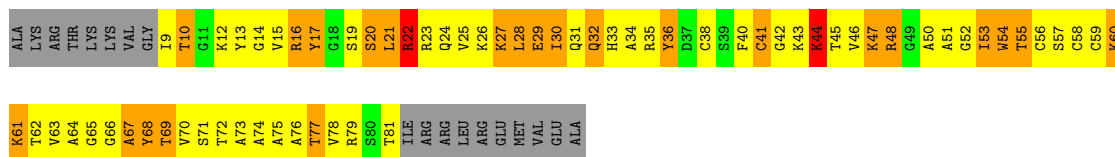
- Molecule 46: 60S ribosomal protein L42

Chain BZ:  13% 51% 20% • 13%



- Molecule 47: 60S ribosomal protein L43

Chain B9:  7% 46% 25% • 20%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of 3D-maps by Wiener filtration	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	4900	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	52000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	AA	0.49	1/35241 (0.0%)	0.77	43/54932 (0.1%)
10	AJ	0.99	0/787	1.17	0/1063
11	AK	1.10	0/936	1.28	3/1260 (0.2%)
12	AL	0.99	0/920	1.19	1/1226 (0.1%)
13	AM	1.06	0/1100	1.54	4/1476 (0.3%)
14	AN	1.13	0/237	1.37	0/315
15	AO	1.09	0/560	1.06	1/745 (0.1%)
16	AQ	1.08	0/631	1.15	0/852
17	AS	1.03	0/636	1.27	3/855 (0.4%)
18	B3	0.58	5/67026 (0.0%)	0.79	89/104457 (0.1%)
19	B4	0.36	0/2905	0.75	4/4528 (0.1%)
2	AT	0.31	0/6496	0.59	1/8794 (0.0%)
20	BA	0.91	0/1706	1.12	1/2289 (0.0%)
21	BB	1.27	2/1889 (0.1%)	4.30	39/2539 (1.5%)
22	BC	1.19	3/2921 (0.1%)	3.76	53/3933 (1.3%)
23	BD	1.46	5/1979 (0.3%)	3.13	28/2680 (1.0%)
24	BE	1.23	1/1840 (0.1%)	1.67	35/2487 (1.4%)
25	BF	1.05	0/1330	1.33	4/1794 (0.2%)
26	BG	1.05	0/895	1.51	15/1208 (1.2%)
27	BH	1.13	0/1429	1.77	18/1925 (0.9%)
28	BI	1.16	0/1352	2.99	29/1815 (1.6%)
29	BJ	1.20	1/1340 (0.1%)	1.89	20/1797 (1.1%)
3	AB	1.00	0/1471	1.13	2/2007 (0.1%)
30	BK	1.08	1/986 (0.1%)	2.52	7/1320 (0.5%)
31	BL	1.33	1/1671 (0.1%)	3.44	43/2239 (1.9%)
32	BM	1.23	1/1190 (0.1%)	3.77	22/1597 (1.4%)
33	BN	1.19	2/1185 (0.2%)	4.05	30/1597 (1.9%)
34	BO	1.20	2/937 (0.2%)	5.64	22/1266 (1.7%)
35	BP	1.24	1/1162 (0.1%)	2.86	20/1550 (1.3%)
36	BQ	1.10	0/811	1.45	7/1081 (0.6%)
37	BR	1.17	0/992	1.52	10/1333 (0.8%)
38	BS	1.23	0/449	1.66	7/597 (1.2%)
39	BT	1.19	0/621	1.52	5/837 (0.6%)
4	AC	1.04	0/1488	1.19	4/1996 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	BU	1.15	0/922	1.78	6/1232 (0.5%)
41	BV	1.08	0/1162	1.32	6/1556 (0.4%)
42	B0	1.18	1/897 (0.1%)	4.22	12/1201 (1.0%)
43	BW	1.17	0/664	1.46	3/885 (0.3%)
44	BX	1.10	0/463	1.44	3/619 (0.5%)
45	BY	1.35	1/412 (0.2%)	6.06	13/548 (2.4%)
46	BZ	1.15	2/752 (0.3%)	7.19	34/995 (3.4%)
47	B9	1.27	0/553	1.66	6/740 (0.8%)
5	AD	1.06	0/1443	1.21	2/1932 (0.1%)
6	AE	1.03	0/1112	1.17	0/1500
7	AG	1.06	0/1169	1.14	2/1570 (0.1%)
8	AH	0.99	0/1021	1.15	0/1371
9	AI	1.18	5/1114 (0.4%)	1.65	21/1492 (1.4%)
All	All	0.77	35/158803 (0.0%)	1.54	678/236031 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	4	37
18	B3	19	47
19	B4	2	0
21	BB	0	2
22	BC	0	1
28	BI	0	2
29	BJ	0	1
30	BK	0	1
31	BL	0	1
32	BM	0	2
33	BN	0	1
34	BO	0	2
35	BP	0	1
38	BS	0	1
40	BU	0	1
41	BV	0	1
47	B9	0	1
All	All	25	102

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	B3	1206	C	O3'-P	-58.99	0.90	1.61
18	B3	2133	U	O3'-P	-56.48	0.93	1.61
18	B3	2168	G	O3'-P	-32.11	1.22	1.61
23	BD	64	TRP	CD2-CE2	-26.50	1.09	1.41
23	BD	64	TRP	NE1-CE2	20.96	1.64	1.37

The worst 5 of 678 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BC	297	PHE	CZ-CE2-CD2	-87.49	15.11	120.10
42	B0	46	PHE	CZ-CE2-CD2	-87.16	15.51	120.10
45	BY	26	PHE	CZ-CE2-CD2	-87.13	15.54	120.10
21	BB	15	PHE	CZ-CE2-CD2	-87.10	15.57	120.10
34	BO	94	PHE	CD1-CE1-CZ	-87.08	15.60	120.10

5 of 25 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	181	G	C3'
1	AA	1493	A	C3'
1	AA	1504	G	C3'
1	AA	1528	U	C3'
18	B3	191	A	C3'

5 of 102 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	12	U	Sidechain
1	AA	197	A	Sidechain
1	AA	203	U	Sidechain
1	AA	231	G	Sidechain
1	AA	51	A	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	31507	0	15705	4692	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AT	6375	0	6431	574	0
3	AB	1438	0	1465	366	0
4	AC	1469	0	1534	306	0
5	AD	1424	0	1448	585	0
6	AE	1099	0	1150	351	0
7	AG	1161	0	1217	318	0
8	AH	1004	0	1033	415	0
9	AI	1094	0	1138	718	0
10	AJ	777	0	828	415	0
11	AK	925	0	935	342	0
12	AL	906	0	955	480	0
13	AM	1084	0	1091	719	0
14	AN	235	0	228	263	0
15	AO	552	0	597	174	0
16	AQ	618	0	655	359	0
17	AS	622	0	625	552	0
18	B3	59964	0	29926	9142	0
19	B4	2600	0	1308	630	0
20	BA	1682	0	1750	644	0
21	BB	1855	0	1912	1147	0
22	BC	2856	0	2895	1961	0
23	BD	1942	0	1964	1382	0
24	BE	1799	0	1710	1194	0
25	BF	1298	0	1365	687	0
26	BG	886	0	953	454	0
27	BH	1410	0	1472	794	0
28	BI	1326	0	1355	735	0
29	BJ	1319	0	1334	777	0
30	BK	978	0	1045	469	0
31	BL	1637	0	1668	873	0
32	BM	1165	0	1243	670	0
33	BN	1163	0	1157	768	0
34	BO	925	0	998	447	0
35	BP	1145	0	1215	793	0
36	BQ	795	0	804	454	0
37	BR	977	0	1008	673	0
38	BS	439	0	445	249	0
39	BT	614	0	635	429	0
40	BU	911	0	987	583	0
41	BV	1133	0	1163	782	0
42	B0	880	0	911	664	0
43	BW	654	0	689	315	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BX	461	0	512	338	0
45	BY	402	0	389	346	0
46	BZ	740	0	798	422	0
47	B9	546	0	556	396	0
All	All	146792	0	101202	29887	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 121.

The worst 5 of 29887 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1329:A:H5'	13:AM:98:TYR:CG	1.25	1.70
18:B3:1694:G:C2	45:BY:5:PRO:HG2	1.20	1.70
18:B3:541:C:C5	42:B0:15:LYS:HG3	1.20	1.69
1:AA:1178:G:P	9:AI:105:LYS:HG2	1.34	1.68
18:B3:2388:C:P	36:BQ:88:ARG:HB3	1.34	1.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AT	811/842 (96%)	779 (96%)	24 (3%)	8 (1%)	18	61
3	AB	183/185 (99%)	159 (87%)	17 (9%)	7 (4%)	4	32
4	AC	186/192 (97%)	169 (91%)	7 (4%)	10 (5%)	2	25
5	AD	176/179 (98%)	157 (89%)	15 (8%)	4 (2%)	7	43
6	AE	145/149 (97%)	134 (92%)	8 (6%)	3 (2%)	8	45
7	AG	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	13	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AH	125/129 (97%)	113 (90%)	6 (5%)	6 (5%)	2	28
9	AI	137/142 (96%)	118 (86%)	11 (8%)	8 (6%)	2	24
10	AJ	95/100 (95%)	80 (84%)	7 (7%)	8 (8%)	1	15
11	AK	123/136 (90%)	110 (89%)	10 (8%)	3 (2%)	7	42
12	AL	116/118 (98%)	101 (87%)	9 (8%)	6 (5%)	2	26
13	AM	127/132 (96%)	121 (95%)	5 (4%)	1 (1%)	22	67
14	AN	27/36 (75%)	23 (85%)	2 (7%)	2 (7%)	1	18
15	AO	63/65 (97%)	60 (95%)	2 (3%)	1 (2%)	11	51
16	AQ	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
17	AS	78/80 (98%)	70 (90%)	7 (9%)	1 (1%)	14	56
20	BA	207/217 (95%)	193 (93%)	9 (4%)	5 (2%)	7	42
21	BB	242/253 (96%)	163 (67%)	48 (20%)	31 (13%)	0	6
22	BC	357/386 (92%)	268 (75%)	55 (15%)	34 (10%)	1	14
23	BD	254/361 (70%)	182 (72%)	42 (16%)	30 (12%)	0	7
24	BE	220/222 (99%)	166 (76%)	31 (14%)	23 (10%)	0	10
25	BF	159/162 (98%)	118 (74%)	27 (17%)	14 (9%)	1	15
26	BG	117/119 (98%)	80 (68%)	21 (18%)	16 (14%)	0	6
27	BH	176/191 (92%)	113 (64%)	36 (20%)	27 (15%)	0	4
28	BI	163/168 (97%)	106 (65%)	43 (26%)	14 (9%)	1	15
29	BJ	163/173 (94%)	113 (69%)	32 (20%)	18 (11%)	0	10
30	BK	127/131 (97%)	117 (92%)	7 (6%)	3 (2%)	7	42
31	BL	192/203 (95%)	128 (67%)	39 (20%)	25 (13%)	0	6
32	BM	144/146 (99%)	106 (74%)	24 (17%)	14 (10%)	1	13
33	BN	145/183 (79%)	101 (70%)	27 (19%)	17 (12%)	0	8
34	BO	118/120 (98%)	82 (70%)	25 (21%)	11 (9%)	1	14
35	BP	139/142 (98%)	89 (64%)	30 (22%)	20 (14%)	0	5
36	BQ	95/100 (95%)	73 (77%)	13 (14%)	9 (10%)	1	14
37	BR	129/137 (94%)	92 (71%)	23 (18%)	14 (11%)	0	10
38	BS	51/56 (91%)	36 (71%)	8 (16%)	7 (14%)	0	6
39	BT	75/83 (90%)	53 (71%)	13 (17%)	9 (12%)	0	7
40	BU	113/126 (90%)	82 (73%)	15 (13%)	16 (14%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BV	141/148 (95%)	102 (72%)	23 (16%)	16 (11%)	0	8
42	B0	107/130 (82%)	76 (71%)	17 (16%)	14 (13%)	0	6
43	BW	76/112 (68%)	57 (75%)	13 (17%)	6 (8%)	1	17
44	BX	57/120 (48%)	41 (72%)	9 (16%)	7 (12%)	0	7
45	BY	50/87 (58%)	35 (70%)	6 (12%)	9 (18%)	0	3
46	BZ	89/105 (85%)	66 (74%)	17 (19%)	6 (7%)	1	21
47	B9	71/91 (78%)	43 (61%)	17 (24%)	11 (16%)	0	4
All	All	6591/7183 (92%)	5282 (80%)	813 (12%)	496 (8%)	2	18

5 of 496 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AT	106	PRO
2	AT	108	HIS
2	AT	460	ASP
3	AB	23	LEU
3	AB	27	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AT	697/715 (98%)	677 (97%)	20 (3%)	48	73
3	AB	153/153 (100%)	146 (95%)	7 (5%)	31	62
4	AC	152/155 (98%)	140 (92%)	12 (8%)	14	45
5	AD	148/149 (99%)	136 (92%)	12 (8%)	14	44
6	AE	115/115 (100%)	109 (95%)	6 (5%)	27	59
7	AG	123/123 (100%)	115 (94%)	8 (6%)	20	52
8	AH	108/110 (98%)	102 (94%)	6 (6%)	25	57
9	AI	116/118 (98%)	111 (96%)	5 (4%)	33	64
10	AJ	91/93 (98%)	82 (90%)	9 (10%)	9	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AK	95/104 (91%)	91 (96%)	4 (4%)	34	64
12	AL	98/98 (100%)	93 (95%)	5 (5%)	28	60
13	AM	116/116 (100%)	113 (97%)	3 (3%)	51	75
14	AN	27/33 (82%)	26 (96%)	1 (4%)	39	68
15	AO	59/59 (100%)	55 (93%)	4 (7%)	18	51
16	AQ	70/70 (100%)	67 (96%)	3 (4%)	33	64
17	AS	66/66 (100%)	63 (96%)	3 (4%)	32	63
20	BA	194/198 (98%)	184 (95%)	10 (5%)	27	59
21	BB	187/195 (96%)	156 (83%)	31 (17%)	2	16
22	BC	299/322 (93%)	252 (84%)	47 (16%)	3	18
23	BD	198/287 (69%)	174 (88%)	24 (12%)	6	27
24	BE	187/187 (100%)	171 (91%)	16 (9%)	12	42
25	BF	142/143 (99%)	121 (85%)	21 (15%)	3	20
26	BG	92/92 (100%)	82 (89%)	10 (11%)	7	30
27	BH	159/171 (93%)	136 (86%)	23 (14%)	4	21
28	BI	141/143 (99%)	118 (84%)	23 (16%)	3	17
29	BJ	143/149 (96%)	119 (83%)	24 (17%)	2	16
30	BK	105/105 (100%)	103 (98%)	2 (2%)	62	82
31	BL	167/175 (95%)	126 (75%)	41 (25%)	1	5
32	BM	123/123 (100%)	106 (86%)	17 (14%)	4	23
33	BN	120/145 (83%)	94 (78%)	26 (22%)	1	7
34	BO	98/98 (100%)	85 (87%)	13 (13%)	4	24
35	BP	119/119 (100%)	90 (76%)	29 (24%)	1	5
36	BQ	86/88 (98%)	76 (88%)	10 (12%)	6	28
37	BR	102/105 (97%)	87 (85%)	15 (15%)	3	20
38	BS	46/49 (94%)	37 (80%)	9 (20%)	1	10
39	BT	68/73 (93%)	59 (87%)	9 (13%)	5	24
40	BU	100/109 (92%)	83 (83%)	17 (17%)	2	15
41	BV	114/118 (97%)	88 (77%)	26 (23%)	1	6
42	B0	94/111 (85%)	70 (74%)	24 (26%)	0	5
43	BW	69/96 (72%)	60 (87%)	9 (13%)	5	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	BX	53/105 (50%)	45 (85%)	8 (15%)	3	20
45	BY	42/70 (60%)	34 (81%)	8 (19%)	2	11
46	BZ	80/90 (89%)	66 (82%)	14 (18%)	2	14
47	B9	56/71 (79%)	44 (79%)	12 (21%)	1	8
All	All	5618/6014 (93%)	4992 (89%)	626 (11%)	11	29

5 of 626 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	BH	125	ASN
31	BL	64	ARG
43	BW	55	ASN
28	BI	33	ILE
29	BJ	34	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 189 such sidechains are listed below:

Mol	Chain	Res	Type
21	BB	99	ASN
23	BD	91	ASN
41	BV	88	GLN
21	BB	186	HIS
22	BC	181	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1436/1507 (95%)	215 (14%)	0
18	B3	2756/2999 (91%)	342 (12%)	0
19	B4	121/125 (96%)	17 (14%)	0
All	All	4313/4631 (93%)	574 (13%)	0

5 of 574 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	8	A
1	AA	9	G

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Mol	Chain	Res	Type
1	AA	31	G
1	AA	32	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
18	B3	35
1	AA	25
20	BA	2
6	AE	1
2	AT	1
30	BK	1
13	AM	1

The worst 5 of 66 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	142:G	O3'	143:A	P	21.73

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AT	480:VAL	C	481:MET	N	21.40
1	AA	178:C	O3'	179:A	P	20.38
1	AA	454:C	O3'	455:C	P	14.81
1	B3	1228:C	O3'	1229:C	P	13.08